



SEQUENCE LISTING

<110> Short, Jay M.
Kretz, Keith A.
Gray, Kevin A.
Barton, Nelson Robert
Garrett, James B.
O' Donoghue, Eileen
Mathar, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES
THEREOF

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<140> US 19 66,379

<141> 2001-05-24

<150> US 09 180,515

<151> 2000-01-15

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<161> 1999-05-25

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<171> 1999-04-13

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<181> 1999-03-11

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<191> 1997-04-13

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1

5

10

15

cag caa tct gca ttc gct cag agt gag cag gag atg aag atg gaa agt

96

RECEIVED

NOV 22 2002

TECH CENTER 1600/2900

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Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	
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caa	ctg	atg	cag	gat	gtc	acc	cca	gac	gca	tgg	cca	acc	tgg	ccg	gta	182
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	
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aag	ggc	tgc	ccg	cag	tct	ggt	cag	gtc	ggg	att	att	ggt	gat	gtc	gac	336
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	
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Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	
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gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acc	tcc	agt	ccc	gat	432
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	
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Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	
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aac	gtg	act	gac	ggg	atc	ctc	agc	agg	gca	gga	ggg	tca	att	gct	gac	528
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	
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Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	
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Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	

21
Ant.

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ggc ggc acc cgc tta ttg gat ttg atc atg gca ggc ttg acc ccc cat Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His 290	295	300	912
cca cgc caa aaa cag ggc tat ggt gtg aca tta ccc act tca gta cgg Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu 305	310	315	960
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu 325	330	335	1008
gag ctc aac tgg acc ctt ccc ggt cag ccg gat aac acc cgc coa ggt Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly 340	345	350	1056
ggt gaa ctg gtg ttt gaa cgc tgg ggt cgg cta agc gat aac agc cag Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln 355	360	365	1104
tgg att cag gtt tgg ctg gtc ttc cag act tta cag cag atg cgt gat Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp 370	375	380	1152
aaa acc cgc ctg tca tta aat acc cgc ccc gga gag gtg aaa ctg acc Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr 385	390	395	1200
ctg gca gga tgt gaa gag cga aat ggc cag ggc atg tgt tgg ttg gca Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala 405	410	415	1248
ggt ttt acc caa atc gtg aat gaa gca cgc ata ccc ggc tgc agt ttg Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu 420	425	430	1296
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 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
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 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 50 55 60
 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
 85 90 95
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
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 Gln Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
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 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
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 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
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 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
 165 170 175
 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
 180 185 190
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
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 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
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 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
 225 230 235 240
 Gln Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
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 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400
 Leu Ala Gly Cys Gln Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
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 Arg Ser His His His His His
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K!
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 cctatcgatg aaaggatct taatcccatt tttatctctt ctgattccgt taaccccgcg 241
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tataacogta atagttatag ccgttaactgt aagcgtgtgt ggcgcgttta atcaaaccaat 1680
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tgatccggcg cattagcacc gcatcaggca atcaataatg tcagatatga aaagcggaaa	180
catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg	240

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro

1

5

10

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gac acc caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg	373
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ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc	421
Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala	
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tat ctg gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg	469
Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu	
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Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp	
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gtc gac gag cgt acc cgt aaa aca gcc gaa gcc ttc gcc gcc ggg ctg	565
Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu	
115 120 125	

gca cct gac tgt gca ata acc gta cat acc cag gca gat acc tcc agt	613
Ala Pro Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser	
130 135 140	

ccc gat ccg tta ttt aat cct cta aaa act gcc gtc tgc caa ctg gat	661
Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp	
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aac gcc aac gtg act gac gcc atc ctg agc agg gca gga ggg tca att	709
Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile	
160 165 170	

B1
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ctg abg gag ata ttt ctg ctg caa caa gca cag gga ctg cgg gag cgg Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro 240 245 250	949
ggg tgg gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt Gly Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser 255 260 265 270	997
ttg cat aac gag caa ttt cat ttg cta caa cgg acg cca gag gtt gcc Leu His Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Gln Val Ala 275 280 285	1045
cgc agc cgg gcc acc ccg tta tta gat ttg atc aag aca ggg ttg acg Arg Ser Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr 290 295 300	1093
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cgt gat aaa acc ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa Arg Asp Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys 385 390 395	1381
ctg acc ctg gca gga tgt gaa gag cga aat ggg cag ggc atg tgt tgg	1429

Leu Thr Leu Ala Gly Cys Gln Glu Arg Asn Ala Gln Gly Met Cys Ser
400 405 410

ttg gaa ggt ttt acg caa atc gtg aat gaa gca cgg ata cgg ggg tgc 1477
Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys
415 420 425 430

agt ttg taatgcataa aiaagagcat taagttacct gaatgcctcg aggcctgatga 1533
Ser Leu

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210 8

211 432

212 PPT

213 Escherichia coli

400 8

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
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Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
20 25 30
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
35 40 45
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
50 55 60
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
85 90 95
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
100 105 110
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
115 120 125
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
130 135 140
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
145 150 155 160
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
165 170 175
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
180 185 190
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
195 200 205
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
210 215 220
Arg Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
225 230 235 240
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
245 250 255

B1
Cont

Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 265 275
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 285 295
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His
 290 300 310
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 310 320 330
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 335 345
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 350 360
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 365 375
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 380 390
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 395 405
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 400 410 420
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 425 435 445

410-9

411-1308

412-DNA

413-Artificial Sequence

416-

417-modified phytase enzyme

421-CDS

422-(1)...(1308)

440-9

atg aag gag atc tta atc cca ttt tta tct ctt ctg att cag tta acc 48
 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
 1 5 10 15
 atg caa tct gaa ttc gct cag agt gag ccg gag ctg aag ctg gaa agt 96
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
 20 25 30
 atg ctg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc aag 144
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 35 40 45
 atg ctg atg cag gat gtc acc cca gac gaa tgg cca acc tgg ccg gta 192
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 50 55 60
 aag ctg ggt gag ctg aca cag cga ggt ggt gag cta atc gcc tat ctc 240
 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 gga cat cac tgg cgt cag cgt ctg gta gcc gac gga tgg ctg cct aaa 288
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys

B1
Cat

	85		90	
tgt ggt tgc cgt cag ttt ggt cag ttt ggt att att ggt gat gtt gat				336
Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp				
100		105	110	
gag cgt acc cgt aaa aca ggt gaa ggc ttt ggt ggt ggg ctg gca cct				384
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro				
115		120	125	
gac tgt gca ata acc gta cat acc cag gca gat acg tac agt ccc gat				432
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp				
130		135	140	
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac ggt				480
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala				
145		150	155	160
aac gtg act gac ggt atc ctc gag agg gca gga ggg tca att gct gac				528
Asn Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp				
165		170	175	
ttt acc ggg cat tat caa acg ggt ttt cgc gaa ctg gaa cgg gtg ctt				576
Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu				
180		185	190	
aat ttt cgg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa				624
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu				
195		200	205	
agc tgt tca tta acg cag gca tta cca tgg gaa ctc aag gtg agc ggc				672
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala				
210		215	220	
gac tgt gtc tca tta acc ggt ggt gta agc ctc gca tca atg ctg acc				720
Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr				
225		230	235	240
gag ata ttt ctc ctg caa caa gca cag gga atg cgg gag cgg ggg tgg				768
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp				
245		250	255	
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat				816
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His				
260		265	270	
aac ggc caa ttt gat ttg cta caa cgc agc cca gag gtt ggc cgc agt				864
Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser				
275		280	285	
cgc gcc acc cgg tta tta gat ttg atc aag aca ggc ttg acg ccc cat				912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His				
290		295	300	
cca ccg caa aaa cag ggt tat ggt gtg aca tta ccc act tca gtg ctg				960
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu				
305		310	315	320

tit atc ggc gga gag gat gat gat ggc gga gat ggc ggc gga atg	1108
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
321 340 335	
gaq ctc aac tgg acg ctc ccc ggt cag cag gat aac acg cag cca ggt	1056
Gln Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340 345 355	
ggt gaa atg gtg tit gaa cgc tgg cgt cgg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355 360 365	
ttg att cag gtt tgg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
370 375 380	
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
381 390 395 400	
atc tca gga tgt gaa gag cga aat gcg cag ggc atg tgt tgg ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
405 410 415	
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
420 425 430	
aaa tct cat cta	1308
Arg Ser His Leu	
435	

#210 - 10
 #211 - 436
 #212 - PRT
 #213 - Artificial Sequence

#2.0 -
 #2.3 - modified phytase enzyme

#4.0 - 10
 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
 1 3 10 15
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
 20 25 30
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 35 40 45
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 50 55 60
 Asn Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys
 85 90 95
 Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
 100 105 110

Glu Arg Thr Arg Lys Thr Gly Gln Ala Phe Ala Ala Gly Leu Ala Pro
 115 125 125
 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
 131 135 145
 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
 145 150 155 160
 Asn Val Thr Asp Ala Ile Leu Gln Arg Ala Gly Gly Ser Ile Ala Asp
 165 170 175
 Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Gln Leu Gln Arg Val Leu
 180 185 190
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Gln Lys Gln Asp Glu
 195 200 205
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Gln Leu Lys Val Ser Ala
 210 215 220
 Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
 225 230 235 240
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
 245 250 255
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350
 Gly Gln Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 405 410 415
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430
 Arg Ser His Leu
 435